

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: _____
Searcher: Beverly C 4994
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

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_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ _____ Other CGN

Shears, Beverly

From: Devi, Sarvamangala
Sent: Tuesday, December 09, 2003 12:46 PM
To: Shears, Beverly
Subject: RE: 10/878,781

Beverly:

The correct number should be 09/878,781.

-----Original Message-----

From: Shears, Beverly
Sent: Tuesday, December 09, 2003 9:28 AM
To: Devi, Sarvamangala
Subject: RE: 10/878,781

Pls. re-check this number. No CRF listing avail.

-----Original Message-----

From: Devi, Sarvamangala
Sent: Tuesday, December 09, 2003 7:37 AM
To: Shears, Beverly
Subject: 10/878,781

Beverly:

In application 10/878,781, would you please perform a sequence and an interference search for:

- A. A protein having the amino acid sequence of SEQ ID NO: 4;
- B. A fragment of SEQ ID NO: 4 having 1-336 amino acids; and
- C. An at least 5 amino acid-long peptide of SEQ ID NO: 4.

Thanks.

S. DEVI, Ph.D.
AU 1645
CM1-7E15

Shears, Beverly

From: Devi, Sarvamangala
Sent: Tuesday, December 09, 2003 7:37 AM
To: Shears, Beverly
Subject: 10/878,781

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Thanks.

S. DEVI, Ph.D.
AU 1645
CM1-7E15

RESULT 17

AAW55089

ID AAW55089 standard; Protein; 333 AA.

XX

AC AAW55089;

XX

DT 02-OCT-1998 (first entry)

XX

DE Streptococcus pneumoniae SP0035 protein.

XX

KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
detection; pneumonia; otitis media; meningitis.

XX

OS Streptococcus pneumoniae.

XX

PN W09818930-A2.

XX

PD 07-MAY-1998.

XX

PF 30-OCT-1997; 97WO-US19422.

XX

PR 31-OCT-1996; 96US-0029960.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Choi GH, Bromocky J A, Johnson LS, Kunsch CA;

XX

DR WPI; 1998-272224/24.

XX

DR N-PSDB; AAV27350.

XX

PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
pneumoniae - or their epitope-containing fragments, useful in
PT protective or therapeutic vaccines, and for diagnosis

XX

PS Claim 11; Page 59; 118pp; English.

XX

CC The present sequence represents a protein from Streptococcus pneumoniae.
 CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
 CC can be useful in vaccines for inducing protective antibodies against
 CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
 CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
 CC are used to detect Streptococcus infection (by usual hybridisation or
 CC amplification methods), also for isolating Streptococcus genes or their
 CC allelic variants. The protein can be used similarly to detect specific
 CC antibodies in standard immunoassays, especially for diagnosing or
 CC monitoring infections. Antibodies which bind the protein are used to
 CC detect corresponding antigens, to purify the protein and for passive
 CC immunisation (optionally coupled to a toxin). Vaccines are administered,
 CC e.g. by injection, orally or through the skin, typically at 0.01-1000
 CC (especially 10-300) mu g/ml per dose.

XX

SQ Sequence 333 AA;

Query Match 17.6%; Score 59; DB 19; Length 333;

Best Local Similarity 100.0%; Pred. No: 1.3e-50;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 GLMTTIHAYTGDQMILDGPHRGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDG 231

Db 171 GLMTTIHAYTGDQMILDGPHRGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDG 229

SEQ ID No. 4 fragment

CC antibody to provide targeting to clots. The plasmin receptor may
CC be useful in human or veterinary medicine, for treatment of thrombosis
CC and pulmonary embolism, and for solubilising clots in catheters or
CC shunts.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 336 AA;

Query Match 99.8%; Score 1711; DB 15; Length 336;
Best Local Similarity 99.4%; Pred. No. 1.8e-144;
Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVKVGVNGRIGRIGLAFFRIQNVGVGVETVINDLTDENMLAHLKYDTTQGRFDGTV 60
Db 1 MVKVGVNGRIGRIGLAFFRIQNVGVGVETVINDLTDENMLAHLKYDTTQGRFDGTV 60
Qy 61 KEGGFVNGNFIKVSARDPENIDWATDGVETVLEATGFFAKKEAAEKHLHANGAKKVI 120
Db 61 KEGGFVNGNFIKVSARDPENIDWATDGVETVLEATGFFAKKEAAEKHLHANGAKKVI 120
Qy 121 TAPGGNDVKTVENTNHDILDTETVISCASCTTNCLAPMAKALHDAFGIQGLMTTIIA 180
Db 121 TAPGGNDVKTVENTNHDILDTETVISCASCTTNCLAPMAKALHDAFGIQGLMTTIIA 180
Qy 181 YTGDMILDGPHRGGLRRARAGAAANIVNSTGAAKAIGLVIPELNGKLDGAAQRPVPT 240
Db 181 YTGDMILDGPHRGGLRRARAGAAANIVNSTGAAKAIGLVIPELNGKLDGAAQRPVPT 240
Qy 241 GSVTELVVTLTKNVSVDEINAAKASNDSCFYTEDPIVSSDIVGVSYGSLFDATQTKM 300
Db 241 GSVTELVVTLTKNVSVDEINAAKASNDSCFYTEDPIVSSDIVGVSYGSLFDATQTKM 300
Qy 301 EVDGSQLVKVSVDNEMSYTTLVRLTLEYFAKIAK 336
Db 301 EVDGSQLVKVSVDNEMSYTTLVRLTLEYFAKIAK 336

See ID No. 4.

RESULT 5
AAR56486
ID AAR56486 standard; Protein; 336 AA.

AC AAR56486;

DT 25-MAR-2003 (updated)
DT 22-FEB-1995 (first entry)
XX Plasmin receptor.

XX Plasmin receptor; isolate 64/14; plasmin; alpha-2-antiplasmin;
XX Plasminogen activator; bleeding; reocclusion; thrombosis;
XX pulmonary embolism; clots.

XX Streptococcus pyogenes.

XX US5328996-A.

XX 12-JUL-1994.

XX 10-AUG-1992; 92US-0928462.

XX 29-MAR-1989; 89US-0330849.

XX 16-MAY-1990; 90US-0524411.

XX 10-AUG-1992; 92US-0928462.

XX (UYFL) UNIV FLORIDA RES FOUND INC.

XX Boyle MDP, Broder C, Lottenberg R, Von Mering G;

XX WPI: 1994-225327/27.

XX N-PSDB; AAQ70705.

XX New DNA encoding bacterial plasmin receptor - useful as
XX thrombolytic agents; used with plasminogen activator or bound to
XX plasmin, also useful in vaccines against bacterial infection
XX Claim 1; Column 27-30; 19pp; English.

XX This sequence represents the S. pyogenes plasmin receptor. The DNA
XX encoding this sequence was isolated from the S. pyogenes clinical
XX isolate 64/14. The plasmin receptor has a very high affinity for
XX plasmin which, when bound, retains its enzymatic activity but is not
XX regulated (inhibited) by alpha-2-antiplasmin. The receptor protein,
XX when administered concurrently or sequentially, prolongs the activity
XX of plasminogen activator (PA) so allows a reduction in dose, and thus
XX lowers the risk of bleeding, and may prevent reocclusion of blood
XX vessels. The protein may be coupled to a fibrin-specific monoclonal

RESULT 1
A42963

glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Streptococcus
N;Alternate names: plasmin receptor
C;Species: Streptococcus sp.
C;Date: 10-Mar-1994 #sequence revision 10-Mar-1994 #text_change 03-Jun-2002
C;Accession: A42963; B42963; JH0750
R;Lottenberg, R.; Broder, C.C.; Boyle, M.D.; Kain, S.J.; Schroeder, B.L.; Curtiss III, J. Bacteriol. 174, 5204-5210, 1992
A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a streptococcal plasmin receptor
A;Reference number: A42963; MUID:92355491; PMID:1322883
A;Accession: A42963
A;Molecule type: DNA
A;Residues: 1-336 <LOT>
A;Experimental source: group A, strain 64/14
A;Note: sequence extracted from NCBI backbone (NCBIP:110308)
A;Accession: B42963
A;Molecule type: protein
A;Residues: 2-74;161-164,'X',166-174;187-211,'X',213-217 <LO2>
R;Pancholi, V.; Fischetti, V.A. J. Exp. Med. 176, 415-426, 1992
A;Title: A major surface protein on group A streptococci is a glyceraldehyde-3-phosphate dehydrogenase
A;Reference number: JH0750; MUID:92364544; PMID:1500854
A;Accession: JH0750
A;Molecule type: protein
A;Residues: 2-30,'A',32-40 <PAN>
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
F;152/Active site: Cys #status predicted

Query Match 99.8%; Score 1711; DB 2; Length 336;
Best Local Similarity 99.4%; Pred. No. 4e-116;
Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLKYDTTQGRFDGTVEV	60
Db	1	MVVKVGINGFGRIGRLAFRRIQNIEGVEVTRINDLTDPNMLAHLKYDTTQGRFDGTVEV	60
QY	61	KEGGFEVNGNFIKVSARDPENIDWATDGVLEATGFFAKKEAAEKHLHANGAKKVI	120
Db	61	KEGGFEVNGNFIKVSARDPENIDWATDGVLEATGFFAKKEAAEKHLHANGAKKVI	120
QY	121	TAPGGNDVKTVPFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA	180
Db	121	TAPGGNDVKTVPFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA	180
QY	181	YTGDMILDGPHRGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRPVPT	240
Db	181	YTGDMILDGPHRGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRPVPT	240
QY	241	GSVTELVVTLTKNVSVDENIAAMKAASNDSFGYTEDPIVSSDIVGVSYSGLFDATQTKVM	300
Db	241	GSVTELVVTLTKNVSVDENIAAMKAASNDSFGYTEDPIVSSDIVGVSYSGLFDATQTKVM	300
QY	301	EVDGSQLVKVSWYDNEMSYTAQLVRTLEYFAKIAK	336
Db	301	EVDGSQLVKVSWYDNEMSYTAQLVRTLEYFAKIAK	336